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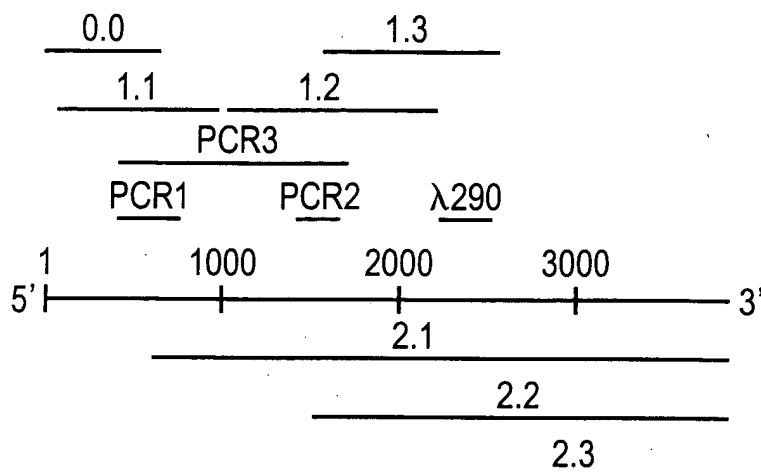


FIG. 1A

PCR Fragm./ CDNA clones	nt. positions
PCR1	388-731
PCR2	1575-1774
PCR3	388-1774
5'RACE	1-540
G6 library	1-641
1.1	53-1007
1.2	1018-2188
1.3	1553-2563
2.1	451-3837
2.2	1590-3983
2.3	2315-3983

FIG. 1B

GGCAGAGGCCGCGGAGGCTGCCGCTCTGGCTTGGCAGTCCCGCGCGCGCTGCACACCGGACCCAGCGCGCTGCCGCGGCGCATGGACCTGCCAGGGGCGCTGGTGGTGCC	120
<u>M D L P R G L V V A</u>	10
TGGGCGCTCAGCCTGTGGCAGGGTTACGGACACCTTCAACATGGACACCAAGAGCCCCGGGTCAATCCCTGGCTCCAGGACCGCCTTCTTTGGCTACACAGTGCAGCAGCAGACATC	240
<u>W A L S L W P G F T D T F N M D T R K P R V I P G S R T A F F G Y T V Q Q H D I</u>	50
AGTGGCAATAAGTGGCTGGTGGCGCCCACTGGAAACCAATGGCTACCAAGACGGGAGACGTGTACAAGTGTCCAGTGTCCAGGGGAACCTGCACCAAACTCAACCTGGGAAGG	360
S G N K W L V V G A P L E T N G Y Q K T G D V Y K C P V I H G N* C T K L N L G R	90
GTCACCCCTGTCCAACGTGTCCGAGCGGAAGACAAACATGGCGCTCGGCCCTTAGTCTGCCACCAACCCCAAGGACAACAGCTTCCTGGCTGCAGCCCCCTCTGGTCTCATGAGTGTGGG	480
V T L S N* V S E R K D N M R L G L S L A T N P K D N S F L A C S P L W S H E C G	130
AGCTCCTACTACACCACAGGGATGTGTTCAAGAGTCAACTCCAACCTTCAGGTTCTCCAAGACCGTGGCCCGCAGCTCTCCAAGGTGCGCAGACCTACATGGACATCGTCTCTGGAT	600
S S Y Y T T G M C S R V N S N F R F S K T V A P A L Q R C Q T Y M D I V I V L D	170
GGCTCCAACAGCATCTACCCCTGGGTGGAGGTTTCAGCACTTCTCATCAACATCCTGAAAAGTTTTACATTTGGCCCGAGGAGATCCAGGTTGGAGTTGTGCAGTATGGCGAAGATGTG	720
G S N S I Y P W V E V Q H F L I N I L K K F Y I G P G Q I Q V G V V Q Y G E D V	210
GTGCATGAGTTTCACCTCAACGACTACAGGTCTGTAAAGATGTGGTGGAAAGCTGCCAGCCACATTTGAGCAGAGAGGAGGAACAGAGACCCGGACGGCATTTGGCATTGAATTTGCACGC	840
V H E F H L N D Y R S V K D V V E A A S H I E Q R G G T E T R T A F G I E F A R	250

SEQ ID No. 1
 FIG. 2A

TCAGAGGCTTCCAGAGGGTGGAGGAAGGAGCCAGAAGGTGATGATTGTTCATCAGATGGGAGTCCACAGACGACCCAGACCTGGAGAAAGGTGATCCAGCAAAAGCGAAAGAGAC 960
S E A F Q K G G R K G A K K V M I V I T D G E S H D S P D L E K V I Q Q S E R D 290

AACGTAACAAGATATGCGGTGGCCGTCCTGGGCTACTACAACCGCAGGGGGATCAATCCAGAAACTTTTCTAAATGAAATCAAATACATCGCCAGTGACCCCTGATGACAAGCACATTCTTTC 1080
N* V T R Y A V A V L G Y Y N R R G I N P E T F L N E I K Y I A S D P D D K H F F 330

AATGTCATGAGGCTGCCTTGAAGGACATTGTGATGCCCTGGGGGACAGAAATCTTCAGCCTGGAAGGCACCAACAAGAACGAGACCTCCTTTGGGCTGGAGATGTCACAGACGGGC 1200
N* V T D E A A L K D I V D A L G D R I F S L E G T N K N* E T S F G L E M S Q T G 370

TTTTCTCGCACGTGGTGAGGATGGGGTTCTGCTGGGAGCCGTCGGTGCCTATGACTGGAATGGAGCTGTGCTAAAGGAGACGAGTGCCGGGGAAGGTCAATTCCTCTCCGCGAGTCCTAC 1320
F S S H V V E D G V L L G A V G A Y D W N G A V L K E T S A G K V I P L R E S Y 410

CTGAAAGAGTTCCTCCGAGGAGCTCAAGAACCATGGTGATACCTGGGGTACACAGTCACATCGGTGCTCCTCCAGGCAGGGGCGAGTGACGTGGCCGGAGCCCCCGGTTCACACCAC 1440
L K E F P E E L K N H G A Y L G Y T V T S V V S S R Q G R V Y V A G A P R F N* H 450

ACGGGCAAGGTCAATCCTGTTACCATGCACAACAACCGGAGCCTCACCATCCACGAGGTATGCGGGGCCAGCAGATAGGCTCTTACTTTGGGAGTGAAATCACCTCGGTGGACATCGAC 1560
T G K V I L F T M H N N* R S L T I H Q A M R G Q Q I G S Y F G S E I T S V D I D 490

GGCGACGGCGTGACTGATGTCTGCTGGTGGCGCACCCCATGTACTTCAACGAGGGCCGCTGAGCGAGGCAAGGTGTACGTCTATGAGCTGAGACAGAACCGGTTTGTATTAAACGGAACG 1680
G D G V T D V L L V G A P M Y F N E G R E R G K V Y V Y E L R Q N R F V Y N* G T 530

SEQ ID No. 1
FIG. 2B

CTAAAGGATTACACAGTTACCGAATGCCGATTGGTGCTCCATTGGCTCAGTTCGAGACCTCAACCAAGGATTCTTACAATGACGTGGTGGGAGCCCCCTGGAGGACAACCCAC 1800
L K D S H S Y Q N A R F G S S I A S V R D L N Q D S Y N D V V V G A P L E D N H 570

GCAGGAGCCATCTACATCTTCCACGGCTTCCGAGGCGAGCATCTCTGAAGACACCTAAGCAGAGAATCACAGCCTCAGAGCTGGCTACCGGCTCCAGTATTTGGCTGCAGCATCCACGGG 1920
A G A I Y I F H G F R G S I L K T P K Q R I T A S E L A T G L Q Y F G C S I H G 610

CAATTGGACCTCAATGAGGATGGGCTCATCGACCTGGCAGTGGGAGCCCTTGGCAACGCTGTGATTCTGTGGTCCCGCCAGTGGTTTCAGATCAATGCCAGCCTCCACTTTGAGCCATCC 2040
Q L D L N E D G L I D L A V G A L G N A V I L W S R P V V Q I N* A S L H F E P S 650

AAGATCAACATCTTCCACAGAGACTGCAAGCGCAGTGGCAGGGATGCCACCTGGCTGGCCGCTTCCCTCTGCTTCACGCCCACTCTTCTGGCACCCCATTTCCAAACAACAACACTGTTGGC 2160
K I N I F H R D C K R S G R D A T C L A A F L C F T P I F L A P H F Q T T T V G 690

ATCAGATACAACGCCACCATGGATGAGAGGCGGTATACACCGAGGCGCCACCTGGACGAGGCGGGGACCGGATTACCAACAAGAGCCGTACTGCTCTCTCCGGCCAGGAGCTCTGTGAG 2280
I R Y N* A T M D E R R Y T P R A H L D E G G D R F T N R A V L L S S G Q E L C E 730

CGGATCAACTTCCATGTCTGGACACTGCTGACTACGTGAAGCCAGTGACCTTCTCAGTCGAGTATTCCTGGAGGACCCTGACCATGGCCCCCATGCTGGACGACGGCTGGCCCCACCACT 2400
R I N F H V L D T A D Y V K P V T F S V E Y S L E D P D H G P M L D D G W P T T 770

CTCAGAGTCTCGGTGCCCTTCTGGAACGGCTGCAATGAGGATGAGCACTGTGTCCCTGACCTTGTGTGGATGCCCCGAGTGACCTGCCACGGCCATGGAGTACTGCCAGAGGGTGCTG 2520
L R V S V P F W N G C N E D E H C V P D L V L D A R S D L P T A M E Y C Q R V L 810

SEQ ID No. 1
FIG. 2C

AGGAAGCCTGCGCAGGACTGCTCCGCATACACGCTGTCCTTCGACACCACAGTCTTCATGAGAGCACACGCCAGCGAGTGGCGGTGGAGGCCACACTGGAGAAACAGGGGCGGAGAAC 2640
R K P A Q D C S A Y T L S F D T T V F I I E S T R Q R V A V E A T L E N R G E N 850

GCCTACAGTACGGTCCCTAAATATCTCGCAGTCAGCAAAACCTGCAGTTTGCCAGCTTGATCCAGAGGAGGACTCAGACGGTAGCATTGAGTGTGTGAACGAGGAGGAGGCTCCAGAAG 2760
A Y S T V L N* I S Q S A N L Q F A S L I Q K E D S D G S I E C V N E E R R L Q K 890

CAAGTCTGCAAGTCAGCTATCCCTTCTTCCGGGCCAAGGCCAAGGTGGCTTTCGGTCTTGATTCGGAGTTCAGCAAAATCCATCTTCTACACCACCTGGAGATCGAGCTCGCTGCAGGC 2880
Q V C N* V S Y P F R A K A K V A F R L D S E F S K S I F L H L E I E L A A G 930

AGTGACAGTAATGAGCGGGACAGCACCAAGGAAGACAACGTGGCCCCCTTACGCTTCCACCTCAAATACGAGGCTGACGTCCCTCTTACCAGGAGCAGCAGCCTGAGCCACTACGAGGTC 3000
S D S N E R D S T K E D N V A P L R F H L K Y E A D V L F T R S S L S H Y E V 970

AAGCTCAACAGCTCGCTGGAGAGATACGATGGTATCGGGCCTCCCTTCAGCTGCATCTTCAGGATCCAGAACTTGGGCTTGTTCCCATCCACGGGATGATGATGAAGATCACCATTCCC 3120
K L N* S S L E R Y D G I G P P F S C I F R I Q N L G L F P I H G M M K I T I P 1010

ATCGCCACCAGGAGCGGCAACCGCTACTGAAGCTGAGGGACTTCCTCAGCGACGAGGCGAACAACGCTCTGTAACTCTGGGGCAATAGCACTGAGTACCGGGCCACCCCGAGTGGAGGAA 3240
I A T R S G N R L L K L R D F L T D E A N* T S C N I W G N* S T E Y R P T P V E E 1050

GACTTGGCTCGTCCACAGCTGAATCACAGCAACTCTGATGTCGTCTCCATCAACTGCAATATACGGCTGGTCCCCAACCCAGGAAATCAATTTCCATCTACTGGGGAACTGTGGTTG 3360
D L R R A P Q L N* H S N S D V V S I N C N I R L V P N Q E I N F H L L G N L W L 1090

SEQ ID No. 1
FIG. 2D

AGGTCCCTAAAAGCACTCAAGTACAAATCCATGAAATCATGGTCAACGCAGCCTTGACAGAGGCAGTTCCACAGCCCTTCATCTTCCGTGAGGAGGATCCCAGCCGCCAGATCGAGTTT 3480
R S L K A L K Y K S M K I M V N A A L Q R Q F H S P F I F R E E D P S R Q I E F 1130

GAGATCTCAAGCAAGAGGACTGGCAGGTCCCCATCTGGATCATTTGTAGGCAGCACCCCTGGGGGGCCCTCTACTGCTGGCCCTGCTGGTCCCTGGCACTGCCGGAAGCTCGGCTTCTTTAGA 3600
E I S K Q E D W Q V P I W I I V G S T L G G L L L A L L V L A L R K L G F F R 1170

AGTGCCAGGCGCAGGAGGAGCCTGGTCTGGACCCCAAGTGTGGAGTGAGGCTCCAGAGGAGACTTTGAGTTGATGGGGGCCAGGACACCACTCCAGGTAGTGTGAGACCC 3720
S A R R R E P G L D P T P K V L E 1188

AGGCCTGTGGCCCCACCGAGCTGGAGCGGAGAGGAAGCCAGCTGGCTTTGCACCTTGACCTCATCTCCCGAGCAATGGCGCCTGCTCCCTCCAGAATGGAACCTCAAGCTGGTTTTAAGTGG 3840

AACTGCCTACTGGGAGACTGGGACACCTTTACACAGACCCCTAGGGATTTAAAGGGACACCCCTACACACAGGCCACGCCAAGGCCCTCCCTCAGGCTCTGTGGAGGGCATTGTGCT 3960

GCCCCAGCTACTAAGGTGCTAGG 3983

SEQ ID No. 1
FIG. 2E

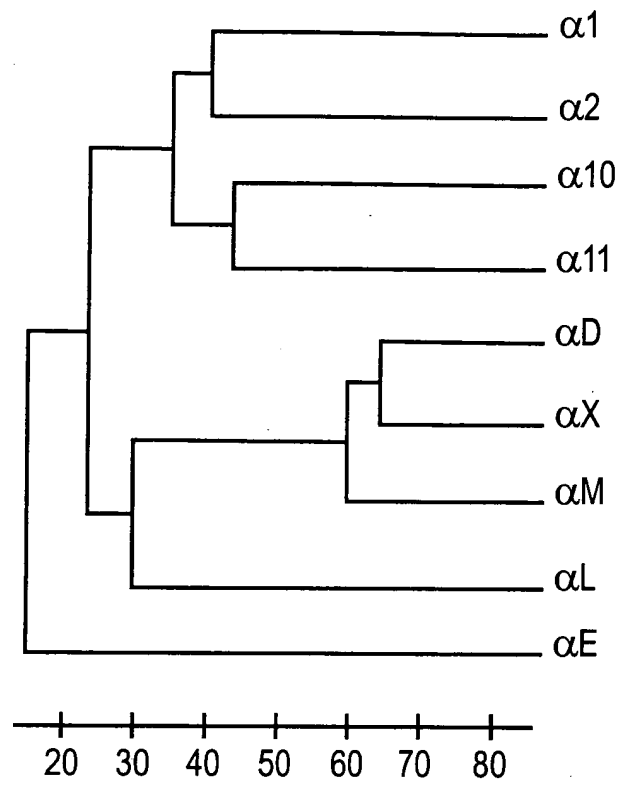


FIG. 3

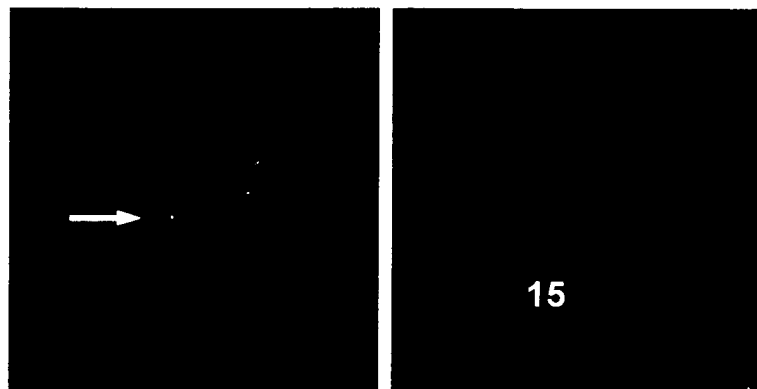


FIG. 4A

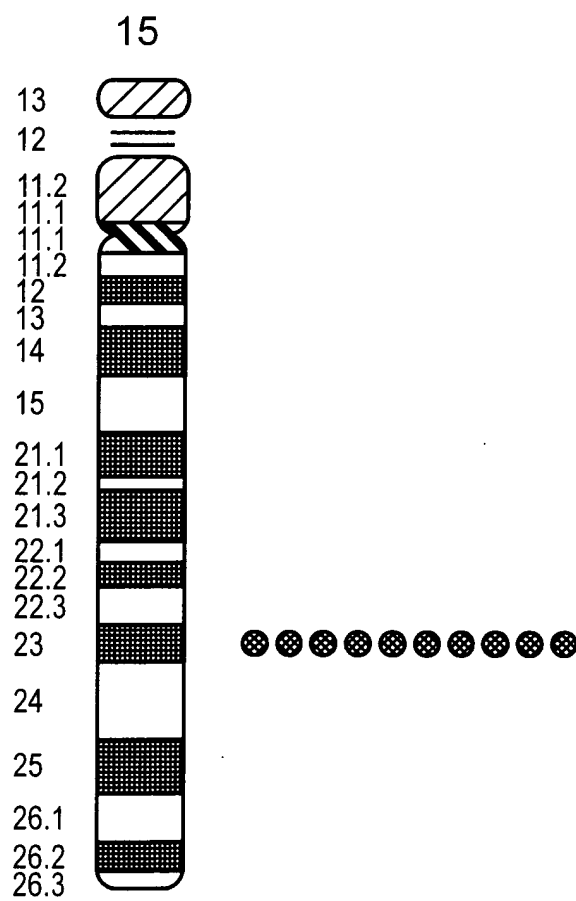


FIG. 4B

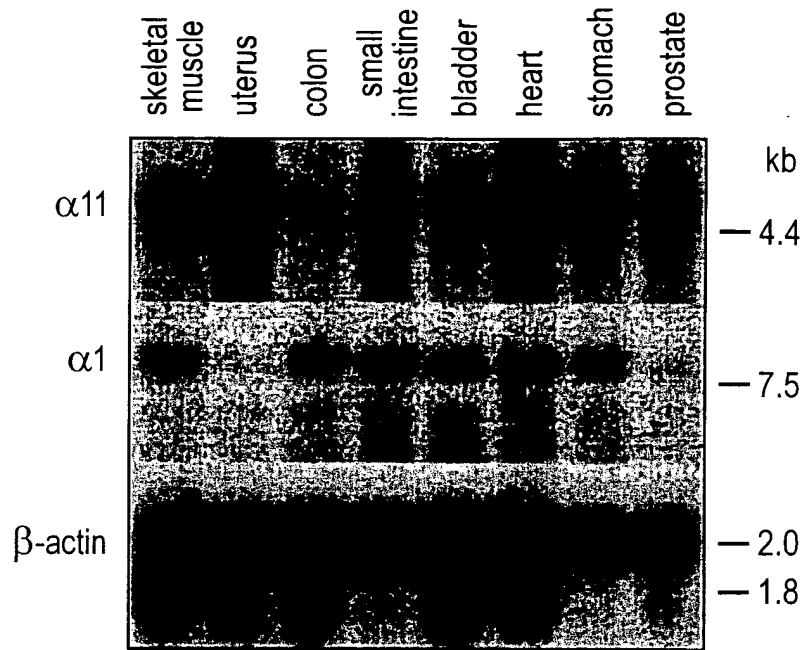


FIG. 5

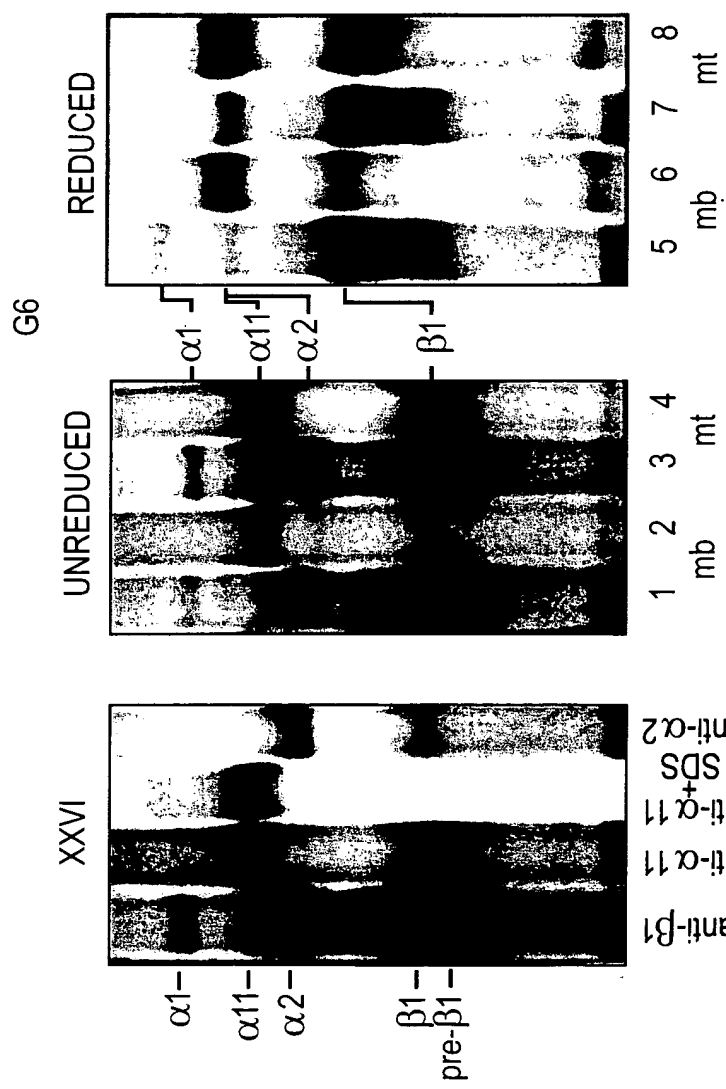


FIG. 6B

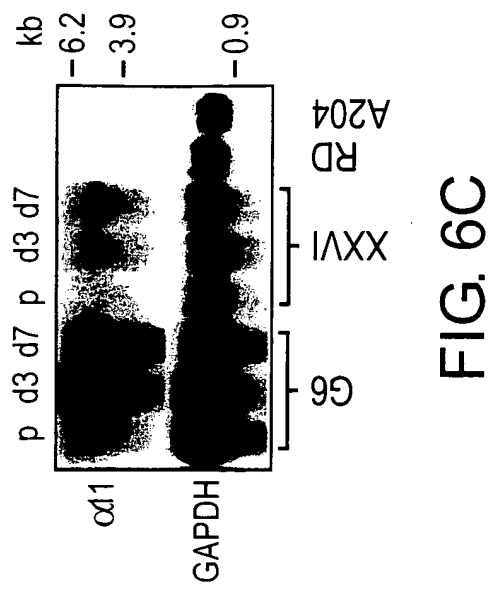


FIG. 6C

FIG. 6A

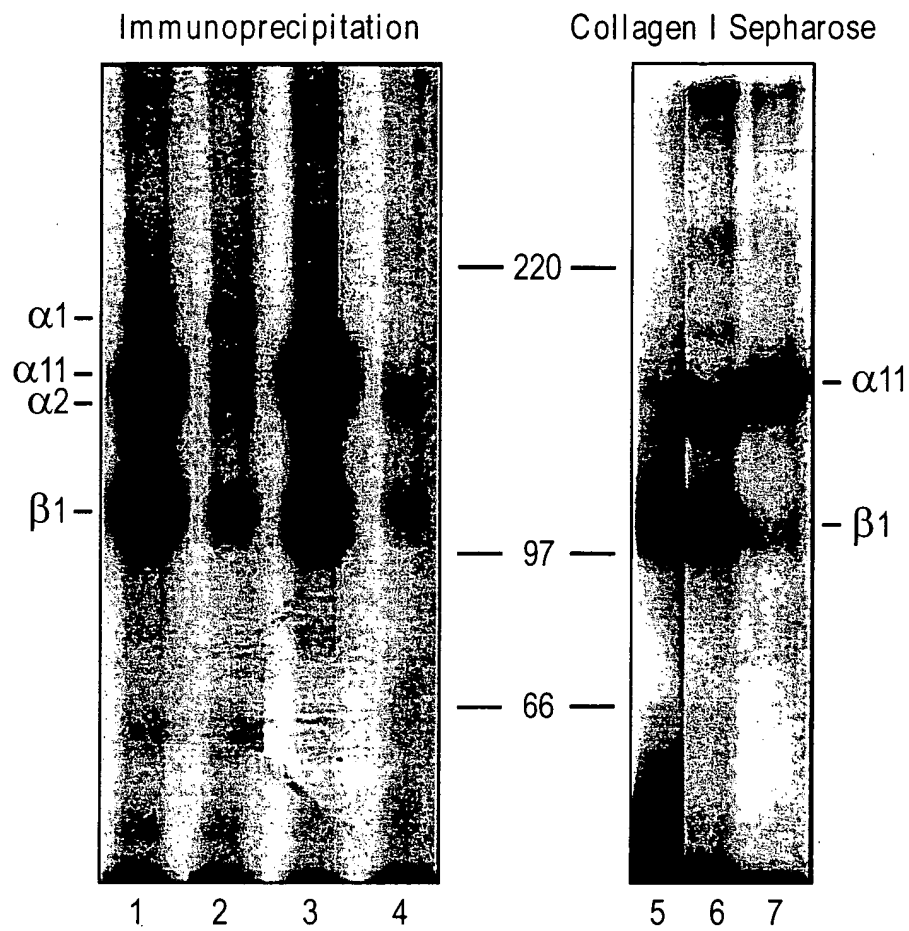


FIG. 7A

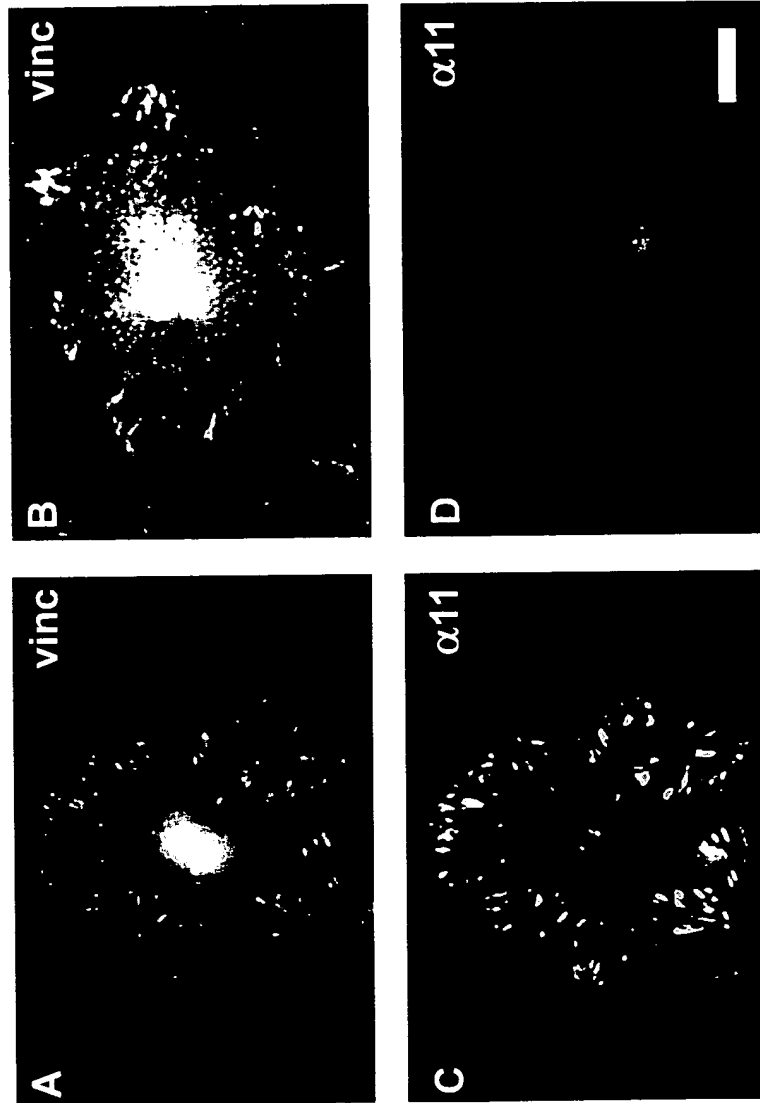


FIG. 7B



FIG. 8

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